RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___10/084,846___

Source: ___OIPE___

Date Processed by STIC: ___4/23/03___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

O IPE

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10 084,846 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ✓ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/084,846

DATE: 04/23/2003
TIME: 12:03:31

Samples errors on pp. 2-6

Input Set : **N:\EBONY'S\EP.txt**
Output Set: **N:\CRF4\04232003\J084846.raw**

```
 3 <110> APPLICANT: Weitnauer, Gabriele
 4         Muhlenweg, Agnes
 5         Trefzer, Axel
 6         Bechthold, Andreas
 8 <120> TITLE OF INVENTION: Avilamycin Derivatives
10 <130> FILE REFERENCE: 1974.005
12 <140> CURRENT APPLICATION NUMBER: US 10/084,846
13 <141> CURRENT FILING DATE: 2002-02-25
15 <150> PRIOR APPLICATION NUMBER: PCT/EP01/09815
16 <151> PRIOR FILING DATE: 2001-08-24
18 <150> PRIOR APPLICATION NUMBER: DE 101 09 166.4
19 <151> PRIOR FILING DATE: 2001-02-25
21 <160> NUMBER OF SEQ ID NOS: 122
23 <170> SOFTWARE: PatentIn Ver. 2.1
```

ERRORED SEQUENCES

```
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 50000
27 <212> TYPE: DNA
28 <213> ORGANISM: Streptomyces viridochromogenes
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Nucleotides 1-50000 of Coding strand 1 of the avilamycin
32         biosynthetic gene cluster of Streptomyces viridochromogenes. The
33         remainder of the nucleotide sequence of coding strand 1 is shown in
34         SEQ ID NO. 2.
37 <400> SEQUENCE: 1
38 ggatccacca tccgtacggc ggcgaacgtc gacagaagct ggatcgacac ggacgcgcgc 60
39 gcgttgttca gcgaccgcct cggcggcctc ccggtgacgg tggtcaacga cgcggacgcg 120
40 gccggcgtcg ccgagatgca cttcggcgcg ggccgcgacc gccggggcac cgtgatcctc 180
41 ctcaccctcg gcacgggcat cggcagcgcg ctgttcatcg acggcgccct ggtccccaac 240
42 acggagctgg gccacctcga actccatggc catgacgccg agaagcgcgc ctccagcaag 300
43 gccagggagg acgaggagct gagctgggag cactgggccc gccgcgtcca gaagtacctc 360
44 gcccatgtcg agatgctgtt ctccccggag ctgttcatca tcggcggcgg ggtgagccgc 420
45 aagtcccaca agttcctgca cctcatcgag ggcatcaagg cggagatcgt cccggcccag 480
46 ctgcagaaca acgccgggat cgtcggggcg gcgatgcggg cggcggagaa ggacggctag 540
47 gccccgcgac gccggggtga tccagacgac agggcctggc ggcggtcacc tggaccggcg 600
48 gcgggccgcg gccctgcggg ccagcagccg gatcttccgt gcggtcacga tgagaccggc 660
49 gatcagcgtc cctccgtaca gccacccggc ctgggtggcg agggcggtga agagccccat 720
50 caggtgtccg ccgatccccc cgccgctgtc ggccaccggc accagcccca cggcgaaggc 780
51 gatcggtacc accaccggcg cggtcgccag gtcgcccctg cgcacccaca ccgccgtcag 840
52 gacgcacacg ggcaggaaca gcacgctgta cagcgtgagc gacgacccga acagcagcga 900
```

RAW SEQUENCE LISTING   DATE: 04/23/2003
PATENT APPLICATION: US/10/084,846   TIME: 12:03:31

Input Set : N:\EBONY'S\EP.txt
Output Set: N:\CRF4\04232003\J084846.raw

wrapped nucleics throughout

-See error summary sheet item 1.

```
      200 gcacagaccg ccaccaccat tggacgccgc ccgggggtgt tccggtccgc agtctctttc 9780
      201 ttgtccacag tcactccagt atggctgcgt tccgccggcg ggggcactcg cgagtgtcag 9840
      202 tcgtcattca tcgtacgaac tgctttctaa gaaatgtgct aaagaatcgg cggctccgac 9900
      203 cgcattggcg ctgttagtct cgaagcgtcg gcctaccaga acgactggac aggtgaggga 9960
E--> 204 tgttggaagc agggcgcctc attcgggcga atgacccggt gctgacctat cgcggcgccg
      205 10020
E--> 206 tctccctcca ggaggtcgac ggtggaatag cgccctggcg aatacctttt caggaacggc
      207 10080
E--> 208 acctgttctt tcccgagggc ggcgtgggac gcgccgcgat gccgacgggg gtgcgggtca
      209 10140
E--> 210 ctttccggac cgacgccgag gggctcgcat tccggtacgc ggcccgtcct gcccccgaga
      211 10200
E--> 212 tgccgggccc gcccgagacg gcgcacgtcg acgtacgagt ggacggcaag ccggtcgcca
      213 10260
E--> 214 gcctccccct ggtgaccgac cgggaggtcc acacgtgccg ggtcggggca ctgccgggcg
      215 10320
E--> 216 gcagcgaccg ccttgtggag ctgtggctgc ccggcctgaa ccagttcgtc ctgcacggcg
      217 10380
E--> 218 tggagttacc ggcaggcgcc gaggtgggcc gggacaccca taccgcgccc cgctgggtcc
      219 10440
E--> 220 actacggggc ctccgagtcg cagggcagag gggcgctgtc gcccacccgg aactggaccg
      221 10500
E--> 222 cgaccgtcgc caccgaactc gggctggacc tgacctcgct ggcgatcggg gcgggctgct
      223 10560
E--> 224 acctccagcc gctcttcgcg accctgctcc gcgacctgcc cgccgatctg atcacgtgca
      225 10620
E--> 226 tggtcggcat gaacatctat ggcgcgcgtg ccctgaacca gttcacctac cggccgaacc
      227 10680
E--> 228 tggtcgggct ggtccggatc atccgggagc gacacccctc gaccccgctg gtcatcgcgt
      229 10740
E--> 230 cccaccacta ctcgccctgg cacgacccgc tggaaggaga cggctacctg tccttgacgg
      231 10800
E--> 232 aggtccggga gcagacccgt gaggtggtcg atctgctgcg cgcggacggc gacgagaacg
      233 10860
E--> 234 tccactacgt ccacggcccg agcctcgccg gccccgaaac cgcccacctg tacgtcgagc
      235 10920
E--> 236 cgcggtacac cgatccgctg cacttcaacc aggaggggca cgacctgctg gcggccgctt
      237 10980
E--> 238 tccagcggaa gctcgtggag ctggtgccgg acctggtgcg gtcctgactc ccggactctc
      239 11040
E--> 240 cccgcaaggc actgcggatc taggaacccg cggacgtatc gggtggatgg tcggatccct
      241 11100
E--> 242 ctgcatcgcc gatgtgtccg ggaagcccgt gggcgaaggc aaccagtccg gcctgaagac
      243 11160
E--> 244 gggattcgac cccgagcttc gccagtatct gggccatatg agccttgacg gtgcgctcgg
      245 11220
E--> 246 tgaccccgag cagcgcggcg atctcacggt tggagtagcc gtggctcagc aggaggaaga
      247 11280
E--> 248 cctggagctc gcggtcggag agtaaatgta cctggctgag cccttccagc caggggaact
```
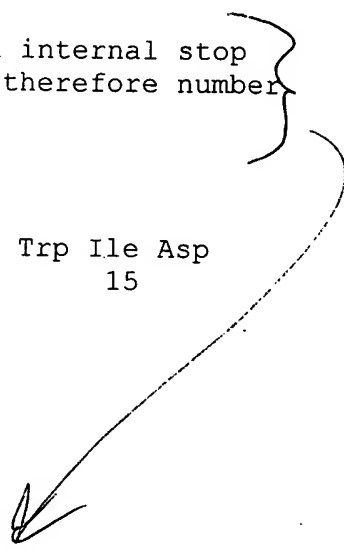
```
        2539 29220
E--> 2540 cagccggagt cggggggcgca gacccgttcg atgatctcga cggtcaactg gtcgtaccag
        2541 29280
E--> 2542 tcgttgagct gggggacggg catctccgtg gccacctcag accgacctct cttcgcgcgc
        2543 29340
E--> 2544 gggcggttgg tccccgctgc cgtccagctc gggcgcgtcg gccagcagtt cgtccagggc
        2545 29400
E--> 2546 gcgcagctcg gcctcgtcga ggtcgaggtc cacggcccgg acgctgtcct ccaggtgctc
        2547 29460
E--> 2548 gggaagctgg gcgccgatga ccgggatgac tcccgagggg tgggccagca cccaggcaag
        2549 29520
E--> 2550 cgcgagctgg gcgacactgt gcccgcgttc ggcggcgaac tccttcagcc ggtccacggc
        2551 29580
E--> 2552 cgcgagcagc ttggcgaagc gttcgccctg gaaggtcggg gagtaggcgc gccagtcgtc
        2553 29640
E--> 2554 gggcgggaac acctggccgg gacggagcgc tcccgccagc accccgtgcg cgagcgccga
        2555 29700
E--> 2556 ccaccccatg acgccgatcc cggcagcggc gcagtgcggc agcacctgct tctcgatgcc
        2557 29760
E--> 2558 gcggtcgagc atgttgaacg gcacctgggc gacctgcggg gtgacgacgg aggagaattc
        2559 29820
E--> 2560 ggccatttcc tcgacggtga agttggagac gcccacgtac cgggcgagcc cttcctccac
        2561 29880
```

<210> 5
<211> 19938
<212> PRT
<213> Streptomyces viridochromogenes

<220>
<223> Protein 1: amino acid sequence encoded by coding strand 1. Start codon: gga, Start position: nucleotide 1.

<220>
<223> Xaa stands, not for an amino acid, but for an internal stop codon in the CDS. The amino acids in the sequence, therefore number only 19,695

<400> 5
Gly Ser Thr Ile Arg Thr Ala Ala Asn Val Asp Arg Ser Trp Ile Asp
 1   5   10   15

Xaa can only represent
an amino acid, and
only a single residue.

See error summary sheet
- Item 5.

<210> 6
<211> 19938
<212> PRT
<213> Streptomyces viridochromogenes

<220>
<223> Protein 2: amino acid sequence encoded by coding strand 1. Start codon: gat, Start position: nucleotide 2.

<220>
<223> Xaa stands, not for an amino acid, but for an internal stop codon in the CDS. The number of amino acids in the sequence, therefore number only 19,725

<400> 6
Asp Pro Pro Ser Val Arg Arg Arg Thr Ser Thr Glu Ala Gly Ser Thr
 1   5   10   15

<210> 7
<211> 19938
<212> PRT
<213> Streptomyces viridochromogenes

<220>
<223> Protein 3: amino acid sequence encoded by coding strand 1. Start codon: atc, Start position: nucleotide 3.

<220>
<223> Xaa stands, not for an amino acid, but for an internal stop codon in the CDS. The number of amino acids in the sequence, therefore number only 19,723

Same Error (handwritten annotation)

<400> 7
Ile His His Pro Tyr Gly Gly Glu Arg Arg Gln Lys Leu Asp Arg His
 1   5   10   15

```
        VARIABLE LOCATION SUMMARY              DATE: 04/23/2003
        PATENT APPLICATION:  US/10/084,846     TIME: 12:03:32

        Input Set : N:\EBONY'S\EP.txt
        Output Set: N:\CRF4\04232003\J084846.raw
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Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

```
Seq#:5; Xaa Pos. 180,552,662,691,744,812,879,951,1134,1163,1179,1215,1293
Seq#:5; Xaa Pos. 1312,1345,1350,1352,1465,1502,1507,1509,1550,1612,1640
Seq#:5; Xaa Pos. 1683,1877,1936,2053,2086,2142,2244,2256,2294,2438,2498
Seq#:5; Xaa Pos. 2534,2576,2660,2688,2707,2969,3037,3290,3294,3335,3350
Seq#:5; Xaa Pos. 3425,3453,3511,3537,3544,3552,3599,3736,3741,3773,3853
Seq#:5; Xaa Pos. 3872,3981,3986,4025,4034,4053,4103,4174,4365,4391,4591
Seq#:5; Xaa Pos. 4891,4962,5008,5096,5141,5202,5204,5214,5299,5314,5361
Seq#:5; Xaa Pos. 5400,5415,5420,5424,5435,5453,5496,5507,5509,5534,5550
Seq#:5; Xaa Pos. 5576,5594,5668,5679,5767,5791,5890,6161,6208,6235,6360
Seq#:5; Xaa Pos. 6374,6522,6544,6575,6593,7173,7217,7222,7225,7261,7324
Seq#:5; Xaa Pos. 7377,7959,7975,7981
Seq#:5; Xaa Pos. 8028,8061,8070,8074,8247,8312,8338,8354,8374,8502,8588
Seq#:5; Xaa Pos. 8726,8831,8878,8889,8953,9151,9170,9183,9232,9509,9837
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Seq#:5; Xaa Pos. 12328,12419,12420,12492,12597,12604,12629,12637,13333
Seq#:5; Xaa Pos. 13374,13387,13441,13469,13481,13491,13546,13561,13609
Seq#:5; Xaa Pos. 13627,13628,13631,13648,13667,13790,13937,14222,14289
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Seq#:5; Xaa Pos. 14591,14615,14617,14621,14627,14671,14688,14719,14764
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Seq#:5; Xaa Pos. 15493,15852,15897,15902
Seq#:5; Xaa Pos. 16058,16113,16132,16165,16193,16242,16280,16289,16657
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Seq#:5; Xaa Pos. 19916
Seq#:6; Xaa Pos. 32,58,107,138,303,461,520,625,947,1050,1097,1125,1236,1250
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Seq#:6; Xaa Pos. 4229,4294,4334,4401,4587,5002,5147,5151,5497,5725,5801
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Seq#:6; Xaa Pos. 8171,8330,8334,8341,8348,8575,8651,8713,8949,9188,9597
Seq#:6; Xaa Pos. 9658,9738,9811,10184,10551,11001,11075,11161,11183,11227
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Seq#:6; Xaa Pos. 13458,13549,13550,13623,13659,13702,14216,14246,14253
Seq#:6; Xaa Pos. 14710,14744,14745,14756,14758,14772,14789,14795,14807
Seq#:6; Xaa Pos. 14813,14818,14899,14911,14946,14983,15442,15504,15559
Seq#:6; Xaa Pos. 15569,15603,15714,15718,15743,15745,15803,15824
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VARIABLE LOCATION SUMMARY   DATE: 04/23/2003
PATENT APPLICATION: **US/10/084,846**   TIME: 12:03:32

Input Set : **N:\EBONY'S\EP.txt**
Output Set: **N:\CRF4\04232003\J084846.raw**

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Seq#:6; Xaa Pos.  16044,16096,16170,16284,16321,16347,16352,16354,16421
Seq#:6; Xaa Pos.  16429,16440,16442,16446,16635,16979,17137,17166,17190
Seq#:6; Xaa Pos.  17270,17309,17551,17592,17714,17731,17746,17797,17821
Seq#:6; Xaa Pos.  17941,18080,18288,18293,18394,18518,18541,18542,18708
Seq#:6; Xaa Pos.  19252,19520,19526,19544,19848,19852,19856,19875,19897
Seq#:7; Xaa Pos.  91,186,217,236,292,403,441,493,892,929,959,971,1036,1060
Seq#:7; Xaa Pos.  1161,1169,1288,1686,1736,1798,1834,1873,1904,2101,2145
Seq#:7; Xaa Pos.  2276,2282,2284,2579,2608,2967,3027,3033,3305,3318,3675
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```
                    VERIFICATION SUMMARY          DATE: 04/23/2003
                    PATENT APPLICATION:  US/10/084,846    TIME: 12:03:32

                    Input Set : N:\EBONY'S\EP.txt
                    Output Set: N:\CRF4\04232003\J084846.raw

L:204 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:10020 SEQ:1
M:254 Repeated in SeqNo=1
L:1898 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:10020 SEQ:3
M:254 Repeated in SeqNo=3
L:3461 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5
L:3461 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5
L:3461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:176
M:341 Repeated in SeqNo=5
L:5302 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:7189 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6
L:7189 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6
L:7189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16
M:341 Repeated in SeqNo=6
L:9059 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:10958 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7
L:10958 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7
L:10958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:80
M:341 Repeated in SeqNo=7
L:12817 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:14704 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8
L:14704 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8
L:14704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:16
M:341 Repeated in SeqNo=8
L:16574 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:18459 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9
L:18459 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9
L:18459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:20333 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:22230 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10
L:22230 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:22230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:64
M:341 Repeated in SeqNo=10
L:24091 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:26182 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:26180
L:26605 M:283 W: Missing Blank Line separator, <220> field identifier
L:27425 M:283 W: Missing Blank Line separator, <400> field identifier
L:31478 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:118
```

This application file contains additional errors !
Only the first 1000 errors are shown above !